

SEQUENCE LISTING

<110> CRACKOWER, MICHAEL A.
PENNINGER, JOSEF M.

<120> COMPOSITIONS AND METHODS FOR TREATING HEART DISEASE

<130> SONN:068US

<140> UNKNOWN

<141> 2005-03-18

<150> PCT/CA2003/001387

<151> 2003-09-19

<150> CA 2,400,254

<151> 2002-09-19

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 3410

<212> DNA

<213> Homo sapiens

<400> 1

atggagctgg agaactataa acagcccgtg gtgctgagag aggacaactg ccgaaggcgc	60
cggaggatga agccgcgcag tgctgcggcc agcctgtcct ccatggagct catccccatc	120
gagttcgtgc tgcccaccag ccagcgcaaa tgcaagagcc ccgaaacggc gctgctgcac	180
gtggccggcc acggcaacgt ggagcagatg aaggcccagg tgtggctgcg agcgctggag	240
accagcgtgg cggcggactt ctaccaccgg ctgggaccgc atcacttcct cctgctctat	300
cagaagaagg ggcagtggta cgagatctac gacaagtacc aggtggtgca gactctggac	360
tgctgcgct actggaaggc cacgcaccgg agcccgggcc agatccacct ggtgcagcgg	420
caccgcacct ccgaggagtc ccaagccttc cagcggcagc tcacggcgct gattggctat	480
gacgtcactg acgtcagcaa cgtgcacgac gatgagctgg agttcacgcg ccgtggcttg	540
gtgaccccg ccatggcgga ggtggccagc cgcgaccca agctctacgc catgcacccg	600
tgggtgacgt ccaagcccct cccggagtac ctgtggaaga agattgcaa caactgcac	660
ttcatcgtca ttcaccgcag caccaccagc cagaccatta aggtctcacc cgacgacacc	720
ccggcgcca tcttcagag cttcttcacc aagatggcca agaagaaatc tctgatggat	780
attcccgaaa gccaaagcga acaggatttt gtgctgcgcg tctgtggccg ggatgagtac	840
ctggtgggcg aaacgcccac caaaaacttc cagtgggtga ggcactgcct caagaacgga	900

gaagagattc acgtggtact ggacacgcct ccagaccggg ccctagacga ggtgaggaag	960
gaagagtggc cgctggtgga cgactgcacg ggagtcaccg gctaccatga gcagcttacc	1020
atccacggca aggaccacga gagtgtgttc accgtgtccc tgtgggactg cgaccgcaag	1080
ttcagggcca agatcagagg cattgatata cccgtcctgc ctcggaacac cgacctcaca	1140
gtttttgtag aggcaaacat ccagcatggg caacaagtcc tttgccaaag gagaaccagc	1200
cccaaaccct tcacagagga ggtgctgtgg aatgtgtggc ttgagttcag tatcaaaatc	1260
aaagacttgc ccaaaggggc tctactgaac ctccagatct actgcggtaa agctccagca	1320
ctgtccagca aggcctctgc agagtcccc agttctgagt ccaagggcaa agttcggctt	1380
ctctattatg tgaacctgct gctgatagac caccgtttcc tcttgcgccg tggagaatac	1440
gtcctccaca tgtggcagat atctgggaag ggagaagacc aaggaagctt caatgctgac	1500
aaactcacgt ctgcaactaa cccagacaag gagaactcaa tgtccatctc cattcttctg	1560
gacaattact gccacccgat agccctgcct aagcatcagc ccacccctga cccggaaggg	1620
gaccgggttc gagcagaaat gcccaaccag cttcgcaagc aattggaggc gatcatagcc	1680
actgatccac ttaaccctct cacagcagag gacaaagaat tgctctggca ttttagatac	1740
gaaagcctta agcaccctaa agcatatcct aagctattta gttcagtga atggggacag	1800
caagaaattg tggccaaaac ataccaattg ttggccagaa ggggaagtctg ggatcaaagt	1860
gctttggatg ttgggttaac aatgcagctc ctggactgca acttctcaga tgaaaatgta	1920
agagccattg cagttcagaa actggagagc ttggaggacg atgatgttct gcattacctt	1980
ctacaattgg tccaggctgt gaaatttgaa ccataccatg atagcgccct tgccagattt	2040
ctgctgaagc gtgggttaag aaacaaaaga attggctact ttttgttttg gttcttgaga	2100
agtgagatag cccagtccag acactatcag cagaggttcg ctgtgattct ggaagcctat	2160
ctgaggggct gtggcacagc catgctgcac gactttaccc aacaagtcca agtaatcgag	2220
atgttacaaa aagtcaccct tgatattaaa tcgctctctg ctgaaaagta tgacgtcagt	2280
tcccaagtta tttcacaact taaacaaaag cttgaaaacc tgcagaattc tcaactcccc	2340
gaaagcttta gagttccata tgatcctgga ctgaaagcag gagcgctggc aattgaaaaa	2400
tgtaaagtaa tggcctccaa gaaaaaacca ctatggcttg agtttaaatg tgccgatcct	2460
acagccctat caaatgaaac aattggaatt atctttaaac atggtgatga tctgcgccaa	2520
gacatgctta ttttacagat tctacgaatc atggagtcta tttgggagac tgaatctttg	2580

gatctatgcc tcctgccata tgggtgcatt tcaactgggtg acaaaatagg aatgatcgag 2640
attgtgaaag acgccacgac aattgccaaa attcagcaaa gcacagtggg caacacggga 2700
gcatttaaag atgaagtcct gaatcactgg ctcaaagaaa aatcccctac tgaagaaaag 2760
tttcaggcag cagtggagag atttgtttat tcctgtgcag gctactgtgt ggcaaccttt 2820
gttcttgga taggcgacag acacaatgac aatattatga tcaccgagac aggaaaccta 2880
tttcatattg acttcgggca cattcttggg aattacaaaa gtttcctggg cattaataaa 2940
gagagagtgc catttgtgct aacccttgac ttcctctttg tgatgggaac ttctggaaag 3000
aagacaagcc cacacttcca gaaatttcag gacatctgtg ttaaggctta tctagccctt 3060
cgtcatcaca caaacctact gatcatcctg ttctccatga tgctgatgac aggaatgccc 3120
cagttaacaa gcaaagaaga cattgaatat atccgggatg ccctcacagt ggggaaaaat 3180
gaggaggatg ctaaaaagta ttttcttgat cagatcgaag tttgcagaga caaaggatgg 3240
actgtgcagt ttaattgggt tctacatctt gttcttgga tcaaacaagg agagaaacat 3300
tcagcctaata actttaggct agaatacaaaa acaagttagt gttctatggt ttaaattagc 3360
atagcaatca tcgaacttgg atttcaaatg caatagacat tgtgaaagct 3410

<210> 2

<211> 1102

<212> PRT

<213> Homo sapiens

<400> 2

Met Glu Leu Glu Asn Tyr Lys Gln Pro Val Val Leu Arg Glu Asp Asn
1 5 10 15

Cys Arg Arg Arg Arg Arg Met Lys Pro Arg Ser Ala Ala Ala Ser Leu
20 25 30

Ser Ser Met Glu Leu Ile Pro Ile Glu Phe Val Leu Pro Thr Ser Gln
35 40 45

Arg Lys Cys Lys Ser Pro Glu Thr Ala Leu Leu His Val Ala Gly His
50 55 60

Gly Asn Val Glu Gln Met Lys Ala Gln Val Trp Leu Arg Ala Leu Glu
65 70 75 80

Thr Ser Val Ala Ala Asp Phe Tyr His Arg Leu Gly Pro His His Phe
85 90 95

Leu Leu Leu Tyr Gln Lys Lys Gly Gln Trp Tyr Glu Ile Tyr Asp Lys
100 105 110

Tyr Gln Val Val Gln Thr Leu Asp Cys Leu Arg Tyr Trp Lys Ala Thr

115					120					125						
His	Arg	Ser	Pro	Gly	Gln	Ile	His	Leu	Val	Gln	Arg	His	Pro	Pro	Ser	
130					135					140						
Glu	Glu	Ser	Gln	Ala	Phe	Gln	Arg	Gln	Leu	Thr	Ala	Leu	Ile	Gly	Tyr	
145					150					155					160	
Asp	Val	Thr	Asp	Val	Ser	Asn	Val	His	Asp	Asp	Glu	Leu	Glu	Phe	Thr	
165					170					175						
Arg	Arg	Gly	Leu	Val	Thr	Pro	Arg	Met	Ala	Glu	Val	Ala	Ser	Arg	Asp	
180					185					190						
Pro	Lys	Leu	Tyr	Ala	Met	His	Pro	Trp	Val	Thr	Ser	Lys	Pro	Leu	Pro	
195					200					205						
Glu	Tyr	Leu	Trp	Lys	Lys	Ile	Ala	Asn	Asn	Cys	Ile	Phe	Ile	Val	Ile	
210					215					220						
His	Arg	Ser	Thr	Thr	Ser	Gln	Thr	Ile	Lys	Val	Ser	Pro	Asp	Asp	Thr	
225					230					235					240	
Pro	Gly	Ala	Ile	Leu	Gln	Ser	Phe	Phe	Thr	Lys	Met	Ala	Lys	Lys	Lys	
245					250					255						
Ser	Leu	Met	Asp	Ile	Pro	Glu	Ser	Gln	Ser	Glu	Gln	Asp	Phe	Val	Leu	
260					265					270						
Arg	Val	Cys	Gly	Arg	Asp	Glu	Tyr	Leu	Val	Gly	Glu	Thr	Pro	Ile	Lys	
275					280					285						
Asn	Phe	Gln	Trp	Val	Arg	His	Cys	Leu	Lys	Asn	Gly	Glu	Glu	Ile	His	
290					295					300						
Val	Val	Leu	Asp	Thr	Pro	Pro	Asp	Pro	Ala	Leu	Asp	Glu	Val	Arg	Lys	
305					310					315					320	
Glu	Glu	Trp	Pro	Leu	Val	Asp	Asp	Cys	Thr	Gly	Val	Thr	Gly	Tyr	His	
325					330					335						
Glu	Gln	Leu	Thr	Ile	His	Gly	Lys	Asp	His	Glu	Ser	Val	Phe	Thr	Val	
340					345					350						
Ser	Leu	Trp	Asp	Cys	Asp	Arg	Lys	Phe	Arg	Val	Lys	Ile	Arg	Gly	Ile	
355					360					365						
Asp	Ile	Pro	Val	Leu	Pro	Arg	Asn	Thr	Asp	Leu	Thr	Val	Phe	Val	Glu	
370					375					380						
Ala	Asn	Ile	Gln	His	Gly	Gln	Gln	Val	Leu	Cys	Gln	Arg	Arg	Thr	Ser	
385					390					395					400	
Pro	Lys	Pro	Phe	Thr	Glu	Glu	Val	Leu	Trp	Asn	Val	Trp	Leu	Glu	Phe	
405					410					415						
Ser	Ile	Lys	Ile	Lys	Asp	Leu	Pro	Lys	Gly	Ala	Leu	Leu	Asn	Leu	Gln	

420					425					430						
Ile	Tyr	Cys	Gly	Lys	Ala	Pro	Ala	Leu	Ser	Ser	Lys	Ala	Ser	Ala	Glu	
435					440					445						
Ser	Pro	Ser	Ser	Glu	Ser	Lys	Gly	Lys	Val	Arg	Leu	Leu	Tyr	Tyr	Val	
450					455					460						
Asn	Leu	Leu	Leu	Ile	Asp	His	Arg	Phe	Leu	Leu	Arg	Arg	Gly	Glu	Tyr	
465					470					475					480	
Val	Leu	His	Met	Trp	Gln	Ile	Ser	Gly	Lys	Gly	Glu	Asp	Gln	Gly	Ser	
485					490					495						
Phe	Asn	Ala	Asp	Lys	Leu	Thr	Ser	Ala	Thr	Asn	Pro	Asp	Lys	Glu	Asn	
500					505					510						
Ser	Met	Ser	Ile	Ser	Ile	Leu	Leu	Asp	Asn	Tyr	Cys	His	Pro	Ile	Ala	
515					520					525						
Leu	Pro	Lys	His	Gln	Pro	Thr	Pro	Asp	Pro	Glu	Gly	Asp	Arg	Val	Arg	
530					535					540						
Ala	Glu	Met	Pro	Asn	Gln	Leu	Arg	Lys	Gln	Leu	Glu	Ala	Ile	Ile	Ala	
545					550					555					560	
Thr	Asp	Pro	Leu	Asn	Pro	Leu	Thr	Ala	Glu	Asp	Lys	Glu	Leu	Leu	Trp	
565					570					575						
His	Phe	Arg	Tyr	Glu	Ser	Leu	Lys	His	Pro	Lys	Ala	Tyr	Pro	Lys	Leu	
580					585					590						
Phe	Ser	Ser	Val	Lys	Trp	Gly	Gln	Gln	Glu	Ile	Val	Ala	Lys	Thr	Tyr	
595					600					605						
Gln	Leu	Leu	Ala	Arg	Arg	Glu	Val	Trp	Asp	Gln	Ser	Ala	Leu	Asp	Val	
610					615					620						
Gly	Leu	Thr	Met	Gln	Leu	Leu	Asp	Cys	Asn	Phe	Ser	Asp	Glu	Asn	Val	
625					630					635					640	
Arg	Ala	Ile	Ala	Val	Gln	Lys	Leu	Glu	Ser	Leu	Glu	Asp	Asp	Asp	Val	
645					650					655						
Leu	His	Tyr	Leu	Leu	Gln	Leu	Val	Gln	Ala	Val	Lys	Phe	Glu	Pro	Tyr	
660					665					670						
His	Asp	Ser	Ala	Leu	Ala	Arg	Phe	Leu	Leu	Lys	Arg	Gly	Leu	Arg	Asn	
675					680					685						
Lys	Arg	Ile	Gly	His	Phe	Leu	Phe	Trp	Phe	Leu	Arg	Ser	Glu	Ile	Ala	
690					695					700						
Gln	Ser	Arg	His	Tyr	Gln	Gln	Arg	Phe	Ala	Val	Ile	Leu	Glu	Ala	Tyr	
705					710					715					720	
Leu	Arg	Gly	Cys	Gly	Thr	Ala	Met	Leu	His	Asp	Phe	Thr	Gln	Gln	Val	

725					730					735					
Gln	Val	Ile	Glu	Met	Leu	Gln	Lys	Val	Thr	Leu	Asp	Ile	Lys	Ser	Leu
			740					745					750		
Ser	Ala	Glu	Lys	Tyr	Asp	Val	Ser	Ser	Gln	Val	Ile	Ser	Gln	Leu	Lys
		755					760					765			
Gln	Lys	Leu	Glu	Asn	Leu	Gln	Asn	Ser	Gln	Leu	Pro	Glu	Ser	Phe	Arg
		770					775					780			
Val	Pro	Tyr	Asp	Pro	Gly	Leu	Lys	Ala	Gly	Ala	Leu	Ala	Ile	Glu	Lys
		785					790					795			800
Cys	Lys	Val	Met	Ala	Ser	Lys	Lys	Lys	Pro	Leu	Trp	Leu	Glu	Phe	Lys
				805					810					815	
Cys	Ala	Asp	Pro	Thr	Ala	Leu	Ser	Asn	Glu	Thr	Ile	Gly	Ile	Ile	Phe
			820					825					830		
Lys	His	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Ile	Leu	Gln	Ile	Leu
		835					840					845			
Arg	Ile	Met	Glu	Ser	Ile	Trp	Glu	Thr	Glu	Ser	Leu	Asp	Leu	Cys	Leu
		850					855					860			
Leu	Pro	Tyr	Gly	Cys	Ile	Ser	Thr	Gly	Asp	Lys	Ile	Gly	Met	Ile	Glu
		865					870					875			880
Ile	Val	Lys	Asp	Ala	Thr	Thr	Ile	Ala	Lys	Ile	Gln	Gln	Ser	Thr	Val
				885					890					895	
Gly	Asn	Thr	Gly	Ala	Phe	Lys	Asp	Glu	Val	Leu	Asn	His	Trp	Leu	Lys
			900					905					910		
Glu	Lys	Ser	Pro	Thr	Glu	Glu	Lys	Phe	Gln	Ala	Ala	Val	Glu	Arg	Phe
		915					920					925			
Val	Tyr	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Thr	Phe	Val	Leu	Gly	Ile
		930					935					940			
Gly	Asp	Arg	His	Asn	Asp	Asn	Ile	Met	Ile	Thr	Glu	Thr	Gly	Asn	Leu
		945					950					955			960
Phe	His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	Asn	Tyr	Lys	Ser	Phe	Leu
				965					970					975	
Gly	Ile	Asn	Lys	Glu	Arg	Val	Pro	Phe	Val	Leu	Thr	Pro	Asp	Phe	Leu
			980					985					990		
Phe	Val	Met	Gly	Thr	Ser	Gly	Lys	Lys	Thr	Ser	Pro	His	Phe	Gln	Lys
		995					1000					1005			
Phe	Gln	Asp	Ile	Cys	Val	Lys	Ala	Tyr	Leu	Ala	Leu	Arg	His	His	
		1010					1015					1020			
Thr	Asn	Leu	Leu	Ile	Ile	Leu	Phe	Ser	Met	Met	Leu	Met	Thr	Gly	

1025		1030		1035
Met Pro Gln Leu Thr Ser Lys Glu Asp Ile Glu Tyr Ile Arg Asp				
1040		1045		1050
Ala Leu Thr Val Gly Lys Asn Glu Glu Asp Ala Lys Lys Tyr Phe				
1055		1060		1065
Leu Asp Gln Ile Glu Val Cys Arg Asp Lys Gly Trp Thr Val Gln				
1070		1075		1080
Phe Asn Trp Phe Leu His Leu Val Leu Gly Ile Lys Gln Gly Glu				
1085		1090		1095
Lys His Ser Ala				
1100				

<210> 3
 <211> 3160
 <212> DNA
 <213> Homo sapiens

<400> 3
 cctccccctcg cccggcgcggtg tcccgtccgc ctctcgctcg cctccccgct cccctcggtc 60
 ttccgaggcg cccgggctcc cggcgcgggcg gcggaggggg cgggcaggcc ggcgggcggt 120
 gatgtggcag gactctttat gcgctgcggc aggatacgcg ctcggcgctg ggacgcgact 180
 gcgctcagtt ctctctctc ggaagctgca gccatgatgg aagtttgaga gttgagccgc 240
 tgtgaggcga ggccgggctc aggcgaggga gatgagagac ggcggcgggc gcggcccgga 300
 gcccctctca gcgctgtga gcagccgcg gggcagcgcc ctcggggagc cggccggcct 360
 gcggcgggcg cagcggcggc gtttctcgcc tctctctcgt cttttctaac cgtgcagcct 420
 cttcctcggc ttctctgaa aggaaggtg gaagccgtgg gctcgggcgg gagccggctg 480
 aggcgcggcg gcggcgggcg cggcacctcc cgctcctgga gcggggggga gaagcggcg 540
 cggcgggcg gcggcgggct gcagctccag ggaggggggtc tgagtcgcct gtcaccattt 600
 ccagggtgga gaacgccgga gagttggtct ctccccttct actgcctcca acacggcggc 660
 ggcggcgggc gcacatccag ggaccgggc cggttttaaa cctcccgtcc gccgcgccc 720
 cccccccgt ggccggggt cgggagggcg ccggcgaggg cagccgttcg gaggattatt 780
 cgtcttctcc ccattccgt gccgcgctg ccaggcctct ggctgctgag gagaagcagg 840
 cccagtcgct gcaaccatcc agcagccgcc gcagcagcca ttaccgggt gcggtccaga 900
 gccaaagcggc ggcagagcga ggggcatcag ctaccgcaa gtccagagcc atttccatcc 960
 tgcagaagaa gccccgccac cagcagcttc tgccatctct ctctccttt ttcttcagcc 1020

acaggctccc	agacatgaca	gccatcatca	aagagatcgt	tagcagaaac	aaaaggagat	1080
atcaagagga	tggattcgac	ttagacttga	cctatatatta	tccaaacatt	attgctatgg	1140
gatttcctgc	agaaagactt	gaaggcgtat	acaggaacaa	tattgatgat	gtagtaaggt	1200
ttttggattc	aaagcataaa	aaccattaca	agatatacaa	tctttgtgct	gaaagacatt	1260
atgacaccgc	caaatttaat	tgcagagttg	cacaatatcc	ttttgaagac	cataaccac	1320
cacagctaga	acttatcaaa	cccttttgtg	aagatcttga	ccaatggcta	agtgaagatg	1380
acaatcatgt	tgcagcaatt	cactgtaaag	ctggaaaggg	acgaactggg	gtaatgatat	1440
gtgcatatth	attacatcgg	ggcaaattth	taaaggcaca	agaggcccta	gatttctatg	1500
gggaagtaag	gaccagagac	aaaaagggag	taactattcc	cagtcagagg	cgctatgtgt	1560
attattatag	ctacctgtta	aagaatcatc	tggattatag	accagtggca	ctgttgthtc	1620
acaagatgat	gtttgaaact	attccaatgt	tcagtggcgg	aacttgcaat	cctcagtttg	1680
tggctctgcca	gctaaaggtg	aagatatatt	cctccaattc	aggaccaca	cgacgggaag	1740
acaagttcat	gtactttgag	ttccctcagc	cgttacctgt	gtgtggtgat	atcaaagtag	1800
agttcttcca	caaacagaac	aagatgctaa	aaaaggacaa	aatgtttcac	ttttgggtaa	1860
atacattctt	cataccagga	ccagaggaaa	cctcagaaaa	agtagaaaat	ggaagtctat	1920
gtgatcaaga	aatcgatagc	atthgcagta	tagagcgtgc	agataatgac	aaggaatatc	1980
tagtacttac	tttaacaaaa	aatgatcttg	acaaagcaaa	taaagacaaa	gccaaccgat	2040
actthtctcc	aaattthtaag	gtgaagctgt	acttcacaaa	aacagtagag	gagccgtcaa	2100
atccagaggc	tagcagttca	acttctgtaa	caccagatgt	tagtgacaat	gaacctgatc	2160
attatagata	ttctgacacc	actgactctg	atccagagaa	tgaaccttht	gatgaagatc	2220
agcatacaca	aattacaaaa	gtctgaattt	thttthtatca	agagggataa	aacaccatga	2280
aaataaaact	gaataaaactg	aaaatggacc	thttththttt	taatggcaat	aggacattgt	2340
gtcagattac	cagttatagg	aacaattctc	thttcttgac	caatcttggt	ttacctata	2400
catccacagg	gtthtgacac	ttgttgcca	gttgaaaaaa	ggttggtgtag	ctgtgtcatg	2460
tatatacctt	thtggtgcaa	aaggacattt	aaaattcaat	taggattaat	aaagatggca	2520
ctthcccgth	ttattccagt	thtataaaaa	gtggagacag	actgatgtgt	atacgtagga	2580
atththtctt	thtggtgtct	gtcaccaact	gaagtggcta	aagagctthg	tgatatactg	2640
gttcacatcc	tacctthtg	cacttgthggc	aacagataag	thtgagttg	gctaagagag	2700

gtttccgaaa ggttttgcta ccattctaata gcatgtattc gggttagggc aatggagggg 2760
 aatgctcaga aaggaaataa ttttatgctg gactctggac catataccat ctccagctat 2820
 ttacacacac ctttcttttag catgctacag ttattaatct ggacattcga ggaattggcc 2880
 gctgtcactg cttgttggtt ggcgattttt ttttaaagca tattggtgct agaaaaggca 2940
 gctaaaggaa gtgaatctgt attgggggtac aggaatgaac cttctgcaac atcttaagat 3000
 ccacaaatga agggatataa aaataatgtc ataggtaaga aacacagcaa caatgactta 3060
 accatataaa tgtggaggct atcaacaaag aatgggcttg aaacattata aaaattgaca 3120
 atgatttatt aaatatgttt tctcaattgt aaaaaaaaaa 3160

<210> 4
 <211> 403
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Thr Ala Ile Ile Lys Glu Ile Val Ser Arg Asn Lys Arg Arg Tyr
 1 5 10 15
 Gln Glu Asp Gly Phe Asp Leu Asp Leu Thr Tyr Ile Tyr Pro Asn Ile
 20 25 30
 Ile Ala Met Gly Phe Pro Ala Glu Arg Leu Glu Gly Val Tyr Arg Asn
 35 40 45
 Asn Ile Asp Asp Val Val Arg Phe Leu Asp Ser Lys His Lys Asn His
 50 55 60
 Tyr Lys Ile Tyr Asn Leu Cys Ala Glu Arg His Tyr Asp Thr Ala Lys
 65 70 75 80
 Phe Asn Cys Arg Val Ala Gln Tyr Pro Phe Glu Asp His Asn Pro Pro
 85 90 95
 Gln Leu Glu Leu Ile Lys Pro Phe Cys Glu Asp Leu Asp Gln Trp Leu
 100 105 110
 Ser Glu Asp Asp Asn His Val Ala Ala Ile His Cys Lys Ala Gly Lys
 115 120 125
 Gly Arg Thr Gly Val Met Ile Cys Ala Tyr Leu Leu His Arg Gly Lys
 130 135 140
 Phe Leu Lys Ala Gln Glu Ala Leu Asp Phe Tyr Gly Glu Val Arg Thr
 145 150 155 160
 Arg Asp Lys Lys Gly Val Thr Ile Pro Ser Gln Arg Arg Tyr Val Tyr
 165 170 175
 Tyr Tyr Ser Tyr Leu Leu Lys Asn His Leu Asp Tyr Arg Pro Val Ala

180					185					190						
Leu	Leu	Phe	His	Lys	Met	Met	Phe	Glu	Thr	Ile	Pro	Met	Phe	Ser	Gly	
195					200					205						
Gly	Thr	Cys	Asn	Pro	Gln	Phe	Val	Val	Cys	Gln	Leu	Lys	Val	Lys	Ile	
210					215					220						
Tyr	Ser	Ser	Asn	Ser	Gly	Pro	Thr	Arg	Arg	Glu	Asp	Lys	Phe	Met	Tyr	
225					230					235					240	
Phe	Glu	Phe	Pro	Gln	Pro	Leu	Pro	Val	Cys	Gly	Asp	Ile	Lys	Val	Glu	
245					250					255						
Phe	Phe	His	Lys	Gln	Asn	Lys	Met	Leu	Lys	Lys	Asp	Lys	Met	Phe	His	
260					265					270						
Phe	Trp	Val	Asn	Thr	Phe	Phe	Ile	Pro	Gly	Pro	Glu	Glu	Thr	Ser	Glu	
275					280					285						
Lys	Val	Glu	Asn	Gly	Ser	Leu	Cys	Asp	Gln	Glu	Ile	Asp	Ser	Ile	Cys	
290					295					300						
Ser	Ile	Glu	Arg	Ala	Asp	Asn	Asp	Lys	Glu	Tyr	Leu	Val	Leu	Thr	Leu	
305					310					315					320	
Thr	Lys	Asn	Asp	Leu	Asp	Lys	Ala	Asn	Lys	Asp	Lys	Ala	Asn	Arg	Tyr	
325					330					335						
Phe	Ser	Pro	Asn	Phe	Lys	Val	Lys	Leu	Tyr	Phe	Thr	Lys	Thr	Val	Glu	
340					345					350						
Glu	Pro	Ser	Asn	Pro	Glu	Ala	Ser	Ser	Ser	Thr	Ser	Val	Thr	Pro	Asp	
355					360					365						
Val	Ser	Asp	Asn	Glu	Pro	Asp	His	Tyr	Arg	Tyr	Ser	Asp	Thr	Thr	Asp	
370					375					380						
Ser	Asp	Pro	Glu	Asn	Glu	Pro	Phe	Asp	Glu	Asp	Gln	His	Thr	Gln	Ile	
385					390					395					400	
Thr Lys Val																